

Notice of Allowability**Application No.**

09/900,237

Examiner

Phuong T. Bui

Applicant(s)

ALLEN, STEPHEN M.

Art Unit

1638

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

All claims being allowable, PROSECUTION ON THE MERITS IS (OR REMAINS) CLOSED in this application. If not included herewith (or previously mailed), a Notice of Allowance (PTOL-85) or other appropriate communication will be mailed in due course. **THIS NOTICE OF ALLOWABILITY IS NOT A GRANT OF PATENT RIGHTS.** This application is subject to withdrawal from issue at the initiative of the Office or upon petition by the applicant. See 37 CFR 1.313 and MPEP 1308.

1. ☒ This communication is responsive to RCE filed 4/15/04.
2. ☒ The allowed claim(s) is/are 23 and 27-35.
3. ☒ The drawings filed on 10/27/03 are accepted by the Examiner.
4. ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
 - a) ☐ All b) ☐ Some* c) ☐ None of the:
 1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

* Certified copies not received: _____.

Applicant has THREE MONTHS FROM THE "MAILING DATE" of this communication to file a reply complying with the requirements noted below. Failure to timely comply will result in ABANDONMENT of this application.
THIS THREE-MONTH PERIOD IS NOT EXTENDABLE.

5. ☐ A SUBSTITUTE OATH OR DECLARATION must be submitted. Note the attached EXAMINER'S AMENDMENT or NOTICE OF INFORMAL PATENT APPLICATION (PTO-152) which gives reason(s) why the oath or declaration is deficient.
 6. ☐ CORRECTED DRAWINGS (as "replacement sheets") must be submitted.
 - (a) ☐ including changes required by the Notice of Draftsperson's Patent Drawing Review (PTO-948) attached
 - 1) ☐ hereto or 2) ☐ to Paper No./Mail Date _____.
 - (b) ☐ including changes required by the attached Examiner's Amendment / Comment or in the Office action of Paper No./Mail Date _____.
- Identifying indicia such as the application number (see 37 CFR 1.84(c)) should be written on the drawings in the front (not the back) of each sheet. Replacement sheet(s) should be labeled as such in the header according to 37 CFR 1.121(d).
7. ☐ DEPOSIT OF and/or INFORMATION about the deposit of BIOLOGICAL MATERIAL must be submitted. Note the attached Examiner's comment regarding REQUIREMENT FOR THE DEPOSIT OF BIOLOGICAL MATERIAL.

Attachment(s)

1. ☒ Notice of References Cited (PTO-892)
2. ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3. ☒ Information Disclosure Statements (PTO-1449 or PTO/SB/08),
Paper No./Mail Date 4/15/04
4. ☐ Examiner's Comment Regarding Requirement for Deposit
of Biological Material
5. ☐ Notice of Informal Patent Application (PTO-152)
6. ☒ Interview Summary (PTO-413),
Paper No./Mail Date 9/3/04
7. ☒ Examiner's Amendment/Comment
8. ☒ Examiner's Statement of Reasons for Allowance
9. ☐ Other _____.

EXAMINER'S AMENDMENT

1. An examiner's amendment to the record appears below. Should the changes and/or additions be unacceptable to applicant, an amendment may be filed as provided by 37 CFR 1.312. To ensure consideration of such an amendment, it MUST be submitted no later than the payment of the issue fee.

Authorization for this examiner's amendment was given in a telephone interview with Kenneth Joung on September 3, 2004.

The application has been amended as follows:

In claim 23, line 4, "90%" was amended to --95%--.

Claim 26 has been canceled.

REASONS FOR ALLOWANCE

2. The following is an examiner's statement of reasons for allowance: Applicant's earliest filing date for SEQ ID NO:29 encoding SEQ ID NO:30 is July 6, 2001. The prior art teaches a sequence having 94.1% (WO2003000898 (N)), 93.9% (WO200179516 (O)), and 93.8% (WO200009706 (P)) sequence identity with Applicant's SEQ ID NO:30. A copy of the PCT documents will not be sent to Applicant, as the Office believes the attached sequence search results from database N_Geneseq will provide Applicant more useful percent sequence identity information. Because the prior art does not teach or fairly suggest a sequence having 95% sequence identity with Applicant's claimed sequence at the amino acid level, the claimed invention is free of the prior art.

3. Any comments considered necessary by applicant must be submitted no later than the payment of the issue fee and, to avoid processing delays, should preferably

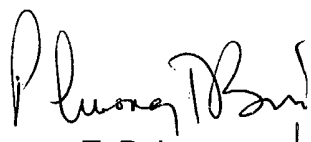
Art Unit: 1638

accompany the issue fee. Such submissions should be clearly labeled "Comments on Statement of Reasons for Allowance."

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Phuong T. Bui whose telephone number is 571-272-0793. The examiner can normally be reached on Monday-Friday.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


Phuong T. Bui
Primary Examiner
Art Unit 1638
9/4/04

9/4/04

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2004, 13:37:22 ; Search time 935 Seconds

(without alignments)
4907.010 Million cell updates/sec

Title: US-09-900-237A-30

Perfect score: 5778

Sequence: 1 MGDADALXSRHGAGDVCO.....VDFPTTLRAGNIQTGNC 1080

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 337863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q/CN2_1/USFTO.spool/US0900237/runat_18082004_081513_14627/app_query.fasta_1.1223
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0900237 @CN 1.1 649 @runat_18082004_081513_14627 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04: *
1: Geneseq1980s: *
2: Geneseq1980s: *
3: Geneseq2000s: *
4: Geneseq2000s: *
5: Geneseq2001bs: *
6: Geneseq2002bs: *
7: Geneseq2003bs: *
8: Geneseq2003bs: *
9: Geneseq2003cs: *
10: Geneseq2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5434.5	94.1	3264	7 ADA69779	ADA69779 Rice gene
2	5423.5	93.9	3799	6 AAS16458	AAS16458 Corn cDNA
3	5421.5	93.8	3746	3 AA299512	AA299512 DNA encod
4	5421.5	93.8	3746	3 AA299527	AA299527 DNA encod
5	5421.5	93.8	3773	3 AA299494	AA299494 DNA encod
6	5169.5	89.5	3222	7 ADA69499	ADA69499 Rice gene
7	5143	89.0	3704	3 AA299533	AA299533 DNA encod
8	4530	78.4	3198	3 AAC49550	AAC49550 Arabidops

9	4499	77.9	3614	2 AAV06567	AAV06567 Arabidops
10	3993.5	69.1	3725	3 AA299500	AA299500 DNA encod
11	3993.5	69.1	3725	3 AA299521	AA299521 DNA encod
12	3993.5	69.1	3725	3 AA299506	AA299506 DNA encod
13	3981	68.9	3753	3 AA299530	AA299530 DNA encod
14	3981	68.9	3753	3 AA299515	AA299515 DNA encod
15	3981	68.9	3780	3 AA299497	AA299497 DNA encod
16	3963.5	68.6	3603	2 AAV06565	AAV06565 Arabidops
17	3953.5	68.4	3673	2 AAV06568	AAV06568 Arabidops
18	3939	68.2	3851	3 AA67114	AA67114 Pinus rad
19	3844.5	66.5	3785	3 AA258265	AA258265 Corn cell
20	3844.5	66.5	3813	3 AA299509	AA299509 DNA encod
21	3844.5	66.5	3813	3 AA299524	AA299524 DNA encod
22	3820	66.1	3568	3 AA299491	AA299491 DNA encod
23	3818	66.1	3776	3 AA258263	AA258263 Corn cell
24	3818	66.1	3936	3 AA258266	AA258266 Corn cell
25	3818	66.1	3969	3 AA299518	AA299518 DNA encod
26	3818	66.1	3969	3 AA299503	AA299503 DNA encod
27	3807.5	65.9	3517	3 AA258268	AA258268 Soybean c
28	3777.5	65.4	3311	2 AAV08373	AAV08373 Cellulose
29	3665.5	63.5	3255	6 AB212754	AB212754 Arabidops
30	3636	62.9	3255	6 AB214725	AB214725 Arabidops
31	3633.5	62.9	3828	2 AAV06566	AAV06566 Arabidops
32	3583	62.0	3444	4 AAC83798	AAC83798 Arabidops
33	3535	61.2	2830	6 AAS16455	AAS16455 Corn cDNA
34	3518.5	60.9	8411	2 AAV06563	AAV06563 Arabidops
35	3514.5	60.8	7234	4 AAC83247	AAC83247 Cellulose
36	3482	60.3	3207	2 AAV08372	AAV08372 Cellulose
37	3477	60.2	3328	2 AAV34432	AAV34432 Cotton ce
38	3461.5	59.9	3747	3 AA67145	AA67145 Eucalyptu
39	3337.5	57.8	3232	4 AAC55448	AAC55448 Populus t
40	3234	56.0	2890	3 AA258270	AA258270 Soybean c
41	2820	48.8	2306	2 AA234433	AA234433 Cotton ce
42	2689	46.3	1734	3 AA258271	AA258271 Wheat cel
43	2674	46.3	2033	2 AAV08381	AAV08381 Cellulose
44	2629.5	45.5	2248	2 AAV06562	AAV06562 Arabidops
45	2627.5	45.5	2125	3 AA258269	AA258269 Soybean c

ALIGNMENTS

RESULT 1
ADA69779
ID: ADA69779 standard; DNA; 3264 BP.

XX AC ADA69779;
XX AC
XX DT 20-NOV-2003 (first entry)
XX DE
XX DE Rice gene, SEQ ID 3102.
XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX KW gene; ds.
XX OS Oryza sativa.
XX PN WO2003000898-A1.
XX PD 03-JAN-2003.
XX PF 22-JUN-2001; 2001WO-IB001105.
XX PR 22-JUN-2001; 2001WO-IB001105.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
WPI; 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to

PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX Claim 6; SEQ ID NO 3102; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

SQ Sequence 3264 BP; 784 A; 751 C; 852 G; 877 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3264
 Score: 5434.50 Matches: 998
 Percent Similarity: 96.60% Conservative: 52
 Best Local Similarity: 91.81% Mismatches: 30
 Query Match: 94.06% Indels: 7
 DB: Gaps: 2

US-09-900-237A-30 (1-1080) x ADA69779 (1-3264)

QY 1 MetAspGlyValAspAlaLeuLysSerGlyArgHisGlyValAspValCysGln 20
 DB 1 ATGGACGGCGACGGCGATCCGTTGAAGTGGGAGGACGGGAGCGGCGGCGGCGGAG 60
 QY 21 IleCysAlaAspGlyLeuGlyThrLeuAspGlyAspValPheThrAlaCysAspVal 40
 DB 61 ATCTGGCGGCGACGGCGTGGGCGACGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 120
 QY 41 CysArgPheProValCysArgProCysTyrGluHisGluArgGlyGlyThrGlnAla 60
 DB 121 TGGCGGTTCCGGTGTGCGCGCCCTCTACAGATCGAGCGGAGGAGGAGGAGGAGGAGGAG 180
 QY 61 CysLeuGlnCysLysThrLysTyrLysArgHisArgGlySerProAlaIleArgGlyGlu 80
 DB 181 TGCCCCCAGTGAAGACCAAGTACAGCGGCCACAGGGGAGGCGGCGGCGGCGGCGGCGGAG 240
 QY 81 GluGlyAspAspThrAspAlaAspGlySerAspPheAsnTyrProLaseGlyThr 100
 DB 241 GAAGCGGAGATCTATCTGATGATGTCTGATGATGTCTGATGATGTCTGATGATGTCTGATGAT 300
 QY 101 GluAspGlnLysGlnLysIleAlaAspArgMetArgSerTrpArgMetAsnThrGlyGly 120
 DB 301 GCGGACCCAGACAGAGAGATTGCTGATAGATGCGGCGGAGTGGCGGATGATGATGATGATGAT 360
 QY 121 SerGlyAsnValGlyHisProLysTyrAspSerGlyGluIleGlyLeuSerLysTyrAsp 140
 DB 361 GTGGAGAGCGTGGCGCGTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 141 SerGlyGluIleProArgGlyTyrValProSerValThrAsnSerGlnMetSerGlyGlu 160
 DB 421 AGTGGCGAGATCCCTCGGGGATACATCCCTTCACTCACTCACTCACTCACTCACTCACTCACTCA 480
 QY 161 IleProGlyAlaSerProAspHisHisMetMetSerProThrGlyAsnIleSerArgArg 180
 DB 481 ATCCCTGGAGCTTCCCTGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 181 AlaProPheProThrValAsnHisSerProAsnProSerArgGluPheSerClySerIle 200
 DB 541 GTCCATATCCCTATGTAACCAATTCACCAATTCACCAATTCACCAATTCACCAATTCACCAATTC 600
 QY 201 GlyAsnValAlaTrpLysGluArgValAspGlyTrpLysMetLysGlnAspLysGlyAla 220
 DB 601 CGAAATGTTGCTGGGAAGAAAGAGTTGATGCTGGAACTGAGCAAGGAGGAGGAGGAGGAGGAG 660
 QY 221 IleProMetThrAsnGlyThrSerIleAlaProSerGluGlyArgAlaAlaThrAspIle 240

DB 661 ATTCCCATGACCAACGGGACAAAGCATTTGCCCTCTCTGAAGGTCGGGAGTGGTGATATC 720
 QY 241 AspAlaSerThrGluTyrAsnMetGluAspAlaLeuLeuAsnAspGluThrArgGlnPro 260
 DB 721 GATGATCCCATGATACATATGGAAGATGCGCTTACTGATGATGAACTCCGCAAGCT 780
 QY 261 LeuSerArgLysValProIleAlaSerSerLysIleAsnProTyrArgMetValIleVal 280
 DB 781 CTCTCTAGAAAGTTCCTCTTCATCCAGATAAATCCCTACAGAAATGGTCATTGTT 840
 QY 281 LeuArgLeuValValLeuSerIlePheLeuHisTyrArgLeuThrAsnProValArgAsn 300
 DB 841 CTGGTTGGTGTCTTAAGCATTTCTTCACTACCTACCTATACGAAATCTCTGCGCAAT 900
 QY 301 AlaTyrProLeuTrpLeuSerValIleCysGluIleTrpPheAlaLeuSerTrpIle 320
 DB 901 GCGTATCCGCTCGCTTTTATCTGTATATGTGAGATTGGTTGCTTGTCTGCTGATA 960
 QY 321 LeuAspGlnPheProLysTrpPheProIleAsnArgGluThrTyrLeuAspArgLeuAla 340
 DB 961 TTGGATCAGTTCGGAAGTGGTTTCCATCAACCGTGAACCTTACCTTGATAGGCTGGCA 1020
 QY 341 LeuArgTyrAspArgGluGlyGluProSerGlnLeuAlaAlaValAspIlePheValSer 360
 DB 1021 TTGAGGTATGACAGAGAGGTGAGCATCTCAGTTGGTGTCTGCTTGCATTTTGTGCT 1080
 QY 361 ThrValAspProLeuLysGluProProIleValThrAlaAsnThrValLeuSerIleLeu 380
 DB 1081 ACAGTCAGCCCAAGAGAACTCTCTTTGTTTACTGCCAATACCTGCTGCTCATCTTT 1140
 QY 381 AlaValAspTyrProValAspLysValSerCysTyrValSerAspAspGlyAlaSerMet 400
 DB 1141 GCTGTGATTACCCAGTGGACAAGGCTCTCTGTATGTATCTGACCATGGTGTGCAATG 1200
 QY 401 LeuThrPheAspAlaLeuAlaGluThrSerGlnPheAlaArgLysTrpValProPheVal 420
 DB 1201 CTGACTTTTGTGATGTGGCTGAGACTCTCAGAGTTTGTCTAGAAAGTGGGTTCATTCGTT 1260
 QY 421 LysLysTyrAspIleGluProArgAlaProGluPheTyrPheCysGlnLysIleAspTyr 440
 DB 1261 AAGAAGTATAAATTCAGGCAAGAGCTCTGAGTGTCTTCTCCAGAAAATCGATTAC 1320
 QY 441 LeuLysAspLysValGlnProSerPheValLysAspArgAlaMetLysArgGluTyr 460
 DB 1321 TTGAAGACAAAGTCCACCCCTTCATTTGTAAAGACCGTGTGCCATGAAGAGAGAATAT 1380
 QY 461 GluGluPheLysIleArgIleAsnAlaLeuValSerLysAlaLeuLysValProGluGlu 480
 DB 1381 GAAGATTCAAGATTAGGATAAATGGCTTGTGTCTAAGCCACAGAAAGTCCCGGAGGAG 1440
 QY 481 GlyTrpIleMetGlnAspGlyThrProTrpProGlyAsnAsnThrArgAspHisProGly 500
 DB 1441 GGATGGATCATGCAAGATGCGCACCATGCCAGGAAACAATACTAGGAGCATCTCTGGA 1500
 QY 501 MetIleGlnValPheLeuGlyHisSerGlyGlyLeuAspThrGluGlyAsnGluLeuPro 520
 DB 1501 ATGATTGAGTTTCTTGGTCAAGTGGTGGCTTGTATACGAGGCTTATGAGCTTCCC 1560
 QY 521 ArgLeuValTyrValSerArgGluLysArgProGlyPheGlnHisLysLysAlaGly 540
 DB 1561 CGCTGTCTACGTATCTGTAAGAGCGTCTCTGGGTTTTCAGCACCAAGAGGCTGGT 1620
 QY 541 AlaMetAsnAlaLeuValArgValSerAlaValLeuThrAsnGlyGlnTyrMetLeuAsn 560
 DB 1621 GCGATGATCTCTTGTGTGTCTCAGCTGTGCTTACCAATGGACAGTACATGTGTAAT 1680
 QY 561 LeuAspCysAspHisTyrIleAsnAsnSerLysAlaValArgGluAlaMetCysPheLeu 580
 DB 1681 CTTGATTGTGATCATTACATCAACACAGCAAGGCTCTCGGGAAGCTATGTCTCTCT 1740
 QY 581 MetAspProAsnLeuGlyProGlnValCysTyrValGlnPheProGlnArgPheAspGly 600

Db 1741 ATGATCCAAACCTAGGAGGAGTCTGTTATGTTTCAGTTCCACAAAGGTTTCGATGGT 1800
Qy 601 IleAsnArgAsnAspArgTyrAlaAsnArgAsnThrValPhePheAspIleAsnLeuArg 620
Db 1801 ATTGATAGGAATGATCATGATATGCGAAGACAGACATGTTGTTTTCGATATTAACCTTGAGG 1860
Qy 621 GlyLeuAspGlyIleGlnGlyProValTyrValGlyThrGlyCysValPheAsnArgThr 640
Db 1861 GGTCTTGATGGCATCCAGGACAGTATGTTGGAACTGTTGTTGTTATTCACAGAACT 1920
Qy 641 AlaIleTyrGlyTyrGluProPheIleAlaAlaLysProGly---PheLeuAlaSer 659
Db 1921 GCTCTATATGTTATGAAACCCCAATTAAGCAGAGAAGAAGGAAAGTTCCTGTCATCA 1980
Qy 660 LeuCysGlyGlyLysLysAlaSerLysSerLysLysArgSerSerAspLysLysLys 679
Db 1981 CTATGTTGGGGCAGGAGGAGGAGCAAGTCAAGAGAAGAGGTTCCGACAGAAGAAG 2040
Qy 680 SerAsnLysHisValAspSerSerValProValPheAsnLeuGluAspIleGluGly 699
Db 2041 TCAACAAGCAGCAGTGCAGTGTGTCAGTTCCTCAATCTTGAAGATATAGAGGAGGT 2100
Qy 700 ValGluGlyAlaGlyPheAspAspGluLysSerValLeuMetSerGlnMetSerLeuGlu 719
Db 2101 GTTGAAGGTCCTGGATTCGATGAGAGAAATCACTTCTTATGTTCTCAAAATGAGCTTGGAG 2160
Qy 720 LysArgPheGlyGlnSerAlaAlaPheValAlaSerThrLeuMetGluTyrGlyVal 739
Db 2161 AAGAGATTTGGCCAGTCTGCAGGCTTGTGTCCTCCACTCTCATGGAATATGGTGGTGT 2220
Qy 740 ProGlnSerSerThrProGluSerLeuLeuLysGluAlaIleHisValIleSerCysGly 759
Db 2221 CCTCAATCTGCACACCCCAAGTCTCTTTTGAAGAAGTATCATGATGATAAGTTGTGCG 2280
Qy 760 TyrGluAspLysSerGluTyrGlyThrGlu-----IleGlyTrpIle 773
Db 2281 TATGAGGACAGACCGAATCGGGAACTGGGCTATGCAACTTGCATGATTCGGTGGATC 2340
Qy 774 TyrGlySerValThrGluAspIleLeuThrGlyPheLysMetHisAlaArgGlyTrpArg 793
Db 2341 TAGGTTCTCGTGCACAGAAGATATCTCACTGGATTCAAGATGATCGCGAGGCTGGAGA 2400
Qy 794 SerValTyrCysMetProLysArgProAlaPheLysGlySerAlaProIleAsnLeuSer 813
Db 2401 TCAATCTACTGATGCCAGGCCCGCCAGCTTTCAGGGGTCGTCTCTCAATCAATCTTCA 2460
Qy 814 AspArgLeuAsnGlnValLeuArgTrpAlaLeuGlySerValGluIleLeuPheSerArg 833
Db 2461 GATCGCTTTAACCAGTCTCGGTGGGCATCTGGTTCCTGTTGAAATCTCTTTCAGTCGC 2520
Qy 834 HisCysProLeuTyrGlyTyrGlyGlyArgGlyPheLeuGluArgPheAlaTyr 853
Db 2521 CATTTGCCATATGTTGACGCTATGAGGAGCCCTTAAGTTCTTGGAGATTTGCCCTAC 2580
Qy 854 IleAsnThrThrIleTyrProLeuThrSerLeuProLeuLeuValTyrCysIleLeuPro 873
Db 2581 ATCAACACCACTATTTATCCATGATCATGCCGCTTCTCATATACGTGTTTGGCT 2640
Qy 874 AlaIleCysLeuLeuThrGlyLysPheIleMetProGluIleSerAsnLeuAlaSerIle 893
Db 2641 GCTATCTGTTGCTCACTCGGAGGTTCAFCATCCAGAGATTAGCAACTTGTAGTATT 2700
Qy 894 TrpPheIleAlaLeuPheLeuSerIlePheAlaThrGlyIleLeuGluMetArgTrpSer 913
Db 2701 TGGTTCACTCTCTCTTCAATTTTGGCATCTGGTATCTTGGATGAGTGGAGT 2760
Qy 914 GlyValGlyIleAspGluTrpTrpArgAsnGluGlnPheTrpValIleGlyLysSer 933
Db 2761 GGTGTGGCATCGATGAGTGGTGGAGGAATGAACAGTTCGGTATTGGAGGTATATCT 2820
Qy 934 AlaHisLeuPheAlaValPheGlnGlyLeuLeuLysValLeuAlaGlyIleAspThrAsn 953
Db 2821 GGGCATCTTTTGGCGTCTTCCAGGGTCTCTCAAGGTCCTTGGTATCGACACCAAT 2880

Qy 954 PheThrValThrSerLysAlaAsnAspGluGlyAspPheAlaGluLeuTyrMetPhe 973
Db 2881 TTCACTGTCACTCAAGGCTTCTGATGAAGATGGGACATTGCTGAGCTCTACATGTTT 2940
Qy 974 LysTrpThrThrLeuLeuIleProProThrThrIleIleIleIleAsnMetValGlyVal 993
Db 2941 AAGTGGACAACGCTTCTCATCCACCGACGACCATCTTGATCATTAACCTGGTGGTGT 3000
Qy 994 ValAlaGlyThrSerTyrAlaIleAsnSerGlyTyrGlnSerTrpGlyProLeuPheGly 1013
Db 3001 GTTGTGTTATCTCATACGGGATCAACAGGGCTACCATTCATCGGAGCCGCTCTTGGC 3060
Qy 1014 LysLeuPhePheAlaPheTrpValIleValHisLeuTyrProPheLeuLysGlyLeuMet 1033
Db 3061 AAGTCTCTTCTTGTGCTTCTGGGTGATTGTCACCTTGACCTTCTCTCAAGGGTCTTATG 3120
Qy 1034 GlyArgGlnAsnArgThrProThrIleValIleValTrpAlaValLeuLeuAlaSerIle 1053
Db 3121 GGTGGGCAAAACCCATCCGACCATCTGTTGTTTGGGCAATCTCTTGGGCTTCGATC 3180
Qy 1054 PheSerLeuLeuTrpValArgValAspProPheThrThrArgLeuAlaGlyProAsnIle 1073
Db 3181 TTCTCATTTGTTGGTTCGATCGATCCATTCACACCGTGTGCACCGCCCGCAGATACC 3240
Qy 1074 GlnThrCysGlyIleAsnCys 1080
Db 3241 CAAACAATGGATCAACTGC 3261
RESULT 2
AAS16458 standard; cDNA; 3799 BP.
XX AAS16458 standard; cDNA; 3799 BP.
AC AAS16458;
XX
DT 14-FEB-2002 (first entry)
XX
DE Corn cDNA encoding cellulose synthase Cqrae19/cesa-19.
XX
KW Corn; ss; cellulose synthase; Cdgq45; cesa-3; Cqrae19; cesa-9;
KW stalk quality; improved strand; silage; pericarp; kernel hardening;
KW handling ability; transgenic plant.
XX
OS Zea mays.
FH Key Location/Qualifiers
FT CDS 238..3799
FT /*tag= a
FT /product= "Cellulose synthase"
XX
FN WO200179516-A2.
XX
PD 25-OCT-2001.
XX
XX 12-APR-2001, 2001WO-US011951.
XX
PR 14-APR-2000; 2000US-00550483.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG;
XX
XX WPT: 2002-041338/05.
XX P-FSDB; AAU10496.
XX
XX New cellulose synthase polypeptides and polynucleotides, useful in
XX improving stalk quality or silage, and in increasing concentration of
XX cellulose in the pericarp, hardening the kernel for improved handling
XX ability.
XX
XX Claim 4; Page 80-85; 88pp; English.
XX
XX The invention relates to isolated nucleic acids encoding two cellulose
XX CC

581 MetAspProAsnLeuGlyProGlnValCysTyrValGlnPheProGlnArgPheAspGly 600
1978 ATGGATCTTAACTAGGAGAGTGTCTGTATGTTTCTAGTTTCCCGAGAGTTTCGATGGT 2037
601 IleAspArgAsnAspArgTyrAlaAsnArgAsnThrValPhePheAspIleAsnLeuArg 620
2038 ATTGATAGGAATGATCGATATGCAACAGGAACACCGTGTGTTTTCGATATTAACCTGAGA 2097
621 GlyLeuAspGlyIleGlnGlyProValTyrValGlyThrCysValPheAsnArgThr 640
2098 GGTCTTGATGGCATCAAGGACAGTATTATGTCGGGACATGGCTGTGTTTCAACAGAAC 2157
641 AlaIleTyrGlyTyrGluProProIleLeuAlaLysLysProGlyPheLeuAlaSerLeu 660
2158 GCTCTATATGTTATGAGCCCCCAATTAAAGAAAGAGGGTGTGTTTCTGTCATCACTA 2217
661 CysGlyGlyLysLysAlaSerLysSerLysLysArgSerSerAspLysLysSer 680
2218 TGTGGTGGCAGGAGGAAGGAAGCAATCAAGAAG--GGCTCAGACAGAAAGTCA 2274
681 AsnLysHisValAspSerSerValProValPheAsnLeuGluAspIleGluGlyVal 700
2275 CAGAGCATGTGACAGTCTCTGTCAGTATTCATCTTGAAGATATAGAGGGAGTT 2334
701 GluGlyAlaGlyPheAspAspGluLysSerValLeuMetSerGlnMetSerLeuGluLys 720
2335 GAAGCGCTGGATTTGATGATGAATAATCACTTCTTATGTTCTCAATGAGCTTGGAGAAG 2394
721 ArgPheGlyGlnSerAlaAlaPheValAlaSerThrLeuMetGluTyrGlyValPro 740
2395 AGATTGGCCATCTCGAGCTTTTGTGGTCCACTCTGATGGAATATGGTGGTTCCT 2454
741 GlnSerSerThrProGluSerLeuLysGluAlaIleHisValIleSerCysGlyTyr 760
2455 CAGTCTGCGACTCCAGATCTCTTCTGAAAGAGTATCCATGTCATAAGTTTGGCTAC 2514
761 GluAspLysSerGluThrGlyThrGluIleGlyTyrIleThrGlySerValThrGluAsp 780
2515 GAGGACAGATTGAATGGGAACTGAGATTGGGTGGATCTATGTTTCTGTGACGAAGAT 2574
781 IleLeuThrGlyPheLysMetHisAlaArgGlyTyrArgSerValTyrCysMetProLys 800
2575 ATTCTCACTGGGTTCAGATGACGACGAGGCTGGCGTGCATCTACTGTCATGCTAAG 2634
801 ArgProAlaPheLysGlySerAlaProIleAsnLeuSerAspArgLeuAsnGlnValLeu 820
2635 CGGCCGGCTTCAAGGGATCGGCTCCCATCAATCTCTCAGACCGTCTGAACACAGGTGCTC 2694
821 ArgTyrAlaLeuGlySerValGluIleLeuPheSerArgHisCysProLeuTyrGly 840
2695 CGGTGGGCTCTCGTTCAGTGGAAATCTTTTCAGCCGCATGCCCCCTATGGTACGGG 2754
841 TyrGlyGlyArgLeuLysPheLeuGluArgPheAlaTyrIleAsnThrThrIleTyrPro 860
2755 TACGGAGGAGCGCTGAAGTCTTGGAGAGATTCCGCTACATCAACACCACTATACCG 2814
861 LeuThrSerLeuProLeuValTyrCysIleLeuProAlaIleCysLeuLeuThrGly 880
2815 CTCACGTCCCTCCGCTCTCTATCTACTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2874
881 LysPheIleMetProGluLysSerAsnLeuAlaSerIleTyrPheIleAlaLeuPheLeu 900
2875 AAGTTTCATCATCCAGAGATCAGCACTTCGCTAGTATCTGTTCTATCTCTCTCTCTCATC 2934
901 SerIlePheAlaThrGlyIleLeuGluMetArgTyrSerGlyValGlyIleAspGluTyr 920
2935 TCAATCTTCGACCGGATATCTGGAGATGAGGTGGAGCGGCTGGCATCGACAGTGG 2994
921 TrpArgAsnGluGlnPheTyrValIleGlyIleSerAlaHisLeuPheAlaValPhe 940
2995 TGGAGGAACAGCAGATTCTGGGTTCATCGGAGGATCTCGGCCCATCTTTCGCGCTCTTC 3054

941 GlnGlyLeuLeuLysValLeuAlaGlyIleAspThrAsnPheThrValThrSerLysAla 960
3055 CAGGGCTCTCTCAAGGTGCTTCGGGATCGACACCACTTCAACCGTCACTCCAGGCC 3114
961 AsnAspGluGluGlyAspPheAlaGluLeuTyrMetPheLysTyrThrThrLeuLeuIle 980
3115 TCGGATGAGACGGGAGCTTCGGAGCTGTACATGTTCAAGTGGAGACACTTCTGATC 3174
981 ProProThrThrIleLeuIleIleAsnMetValGlyValValAlaGlyThrSerTyrAla 1000
3175 CCGGCCACCATCTCTGATCATCAAGCTGTGCGGCTGTTGCGGCGCATCTCTACGCC 3234
1001 IleAsnSerGlyTyrGlnSerTyrProLeuPheGlyLysLeuPhePheAlaPheTyr 1020
3235 ATCAACAGCGGTACCACTGTCGGGCTCGCTCTTCGGCAAGCTCTTCTTCTGCTTCTGG 3294
1021 ValIleValHisLeuTyrProPheLeuLysGlyLeuMetGlyArgGlnAsnArgThrPro 1040
3295 GTGATCGTTCACCTGTACCGGTTCTCAAGGTTCTATGGTTCGGCAGAACCGCACCCG 3354
1041 ThrIleValIleValTyrAlaValLeuLeuAlaSerIlePheSerLeuLeuTyrValArg 1060
3355 ACCATCGTGGTGTCTGGGATCTCTGCTGCGTCTCTTCTCTTCTGCTGCTGCTGCTGCTG 3414
1061 ValAspProPheThrThrArgLeuAlaGlyProAsnIleGlnThrCysGlyIleAsnCys 1080
3415 ATCGATCGTTCACCAACCGGTCACCTGCGCGGATCTCGAAGCTGTGGCATCACTGC 3474
RESULT 3
AAZ99512
ID AAZ99512 standard; DNA; 3746 BP.
XX
AC AAZ99512;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a maize cellulose synthase.
XX
KW Maize; cellulose synthase; stalk quality; stand; silage; cellulose;
KW transgenic plant; plant breeding marker; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 321..3548
FT /*tag= a
FT /product= "cellulose synthase"
FT /transl_except= (pos:1800..1802, aa: Xaa)
FT /note= "no termination codon given; Xaa is an unspecified
FT amino acid"
XX
PN MQ390009.9-46-A2.
XX
92 24-FEB-2000.
XX
9F 16-AUG-1999; 99WO-US018760.
XX
9R 17-AUG-1998; 98US-0096822P.
XX
9A (PION-) PIONEER HI-BRED INT INC.
XX
9I Dhugga KS, Helentjaris TC, Bowen BA, Wang X;
XX WPI; 2000-224343/19.
XX P-PSDB; AAY84114.
XX
XX New genes which encode maize cellulose synthase polypeptides in plants
XX useful for modulating the expression of cellulose synthase in plants and
XX to produce transgenic plants expressing the novel protein.
XX Claim 1; Page 137-141; 119pp; English.
XX
XX The present sequence encodes a maize cellulose synthase polypeptide. The

cellulose synthase can be used for the improvement of stalk quality for improved stand or silage. It also provides an increased concentration of cellulose in the pericarp, hardening the kernel and improving its handling ability. The sequences are used to produce transgenic plants and seeds expressing the cellulose synthase. The polynucleotide is used for modulating, preferably increasing, the level of the synthase in a plant cell. The plants are preferably monocots. The polynucleotide is also used as a probe or primer in the detection quantitation or isolation of gene transcripts. The probes are useful in detecting deficiencies in the level of mRNA in screenings for desired transgenic plant, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants of the gene, or for use as molecular markers in plant breeding programs. The isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein

Sequence 3746 BP; 861 A; 976 C; 1006 G; 902 T; 0 U; 1 Other;

Alignment Scores:		
Pred. No.:	0	Length: 3746
Score:	521.50	Matches: 998
Percent Similarity:	96.67%	Conservative: 46
Best Local Similarity:	92.41%	Mismatches: 33
Query Match:	93.83%	Indels: 3
DB:	3	Gaps: 2

US-09-900-237A-30 (1-1080) x AAZ99512 (1-3746)

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Db	321	Ala	GAGGGGG	CGG	CGC	AGC	CGT	GAAGT	CGGGG	AGG	CGCGT	TGGCG	GAC	AGG	TGT	CCAG	380									
Qy	21	Ile	Cys	Ala	Asp	Gly	Leu	Cly	Thr	Thr	Leu	Asp	Gly	Asp	Val	Phe	Thr	Ala	Cys	Asp	Val	40				
Db	381	Ala	TCTGGGG	CGC	AGC	GCG	TGG	CGC	ACC	ACG	CGG	GAG	GGG	GAC	GTCTT	CGCGG	CTCG	CGC	AGT	C	440					
Qy	41	Cys	Arg	Phe	Pro	Val	Cys	Arg	Pro	Cys	Tyr	Glu	His	Gly	Arg	Gly	Ser	Glu	Gly	Thr	Gln	Ala	60			
Db	441	TGC	GGGT	TTT	CCG	GTG	TGC	CGC	CCCT	CTC	TAC	GAG	TAC	GAG	CGC	AC	GAG	CGC	AC	GCG	AGC	GCG	500			
Qy	61	Cys	Leu	Gln	Cys	Iys	Thr	Iys	Tyr	Iys	Arg	His	Arg	Gly	Ser	Pro	Ala	Ile	Arg	Gly	Glu	80				
Db	501	TGC	CCCC	ACG	TGC	AC	AGC	CAAG	TAC	AA	GGC	CGC	AC	AGG	GGG	AGC	CGC	GGG	CGAT	CCG	TGG	GGAG	560			
Qy	81	Glu	Cly	Asp	Asp	Thr	Asp	Ala	Asp	Asp	Gly	Ser	Asp	Phe	Asn	Tyr	Pro	Ala	Ser	Cly	Thr	100				
Db	561	GA	AGG	AG	AC	G	CA	CT	GT	AT	CC	CG	AT	-----	AGC	GAC	TTT	CA	AT	TAC	CT	TGC	CAAT	614		
Qy	101	Glu	Asp	Gln	Lys	Gln	Lys	Ile	Ala	Asp	Arg	Met	Arg	Ser	Trp	Arg	Met	Asn	Thr	Gly	Gly	120				
Db	615	GAG	AC	CA	CA	AG	CGA	AG	ATT	CC	CG	AC	AGA	AT	GCG	AGC	TGG	CG	CA	TGA	AC	CTT	TGGGGC	674		
Qy	121	Ser	Gly	Asn	Val	Gly	His	Pro	Lys	Tyr	Asp	Ser	Gly	Glu	Lle	Gly	Leu	Ser	Lys	Tyr	Asp	140				
Db	675	ACG	CGG	GGAT	GTG	TGT	CGC	CCCA	AGT	AT	AC	AGT	TAC	AGT	TGG	CGAG	AT	CGG	GGC	TTT	AC	CAAGT	ATGAC	734		
Qy	141	Ser	Gly	Glu	Ile	Pro	Arg	Gly	Tyr	Val	Pro	Ser	Val	Thr	Asn	Ser	Gln	Met	Ser	Gly	Glu	160				
Db	735	AGT	GGC	CA	AG	ATT	CTT	CT	CGG	GGAT	TAC	AT	CC	AT	CA	GT	CT	AA	C	CG	CA	AGT	TCT	CAGAGAA	794	
Qy	161	Ile	Pro	Gly	Ala	Ser	Pro	Asp	His	His	Met	Ser	Pro	Thr	Gly	Asn	Ile	Ser	Arg	Arg	180					
Db	795	AT	CC	CT	GGT	GT	CT	CC	CT	GAC	CA	T	CA	T	AT	G	T	AT	G	T	AT	G	T	AT	854	
Qy	181	Ala	Pro	Phe	Pro	Tyr	Val	Asn	His	Ser	Pro	Asn	Pro	Ser	Arg	Glu	Phe	Ser	Gly	Ser	Ile	200				
Db	855	GTC	CA	AT	TT	CC	CT	AT	G	T	GA	CA	AT	T	CG	CA	AT	CC	GT	CA	AGG	AGT	TCT	CTGT	ATGAC	914

1995 CTTGATTGTGATCACTACATTAACAACAGTAAAGGCTCTCAGGAGAGTAATGTCTTCCTT 2054
581 MetAspProAsnLeuGlyProGlnValCysTyrValGlnPheProGlnAArgPheAspGly 600
2055 ATGACCCCTAACCTTAGAAGAGAGTGTCTGTACGTCCAGTTTCCAGAGATTTCGATGCC 2114
601 IleAspArgAsnAspArgTyrAlaAsnArgAsnThrValPhePheAspIleAsnLeuArg 620
2115 ATTGACAGGATGATCATATGCCACAGGAACACCGTGTTTTTCGATATTAACCTTGAGA 2174
621 GlyLeuAspGlyIleGlnGlyProValTyrValGlyThrGlyCysValPheAsnArgThr 640
2175 GGTCTTCATGGCATCCAGCAAGCAAGTATATGTGGAACTGGCTGTGTTTTCAACCGAACA 2234
641 AlaIleTyrGlyTyrGluProProIleValAlaIleLysProGlyPheLeuAlaSerLeu 660
2235 GCTCTATATGTTATGAGCCCAATTAAGCAAGAAGAGGTGTTCTTGTTCATCACTA 2294
661 CysGlyGlyLysLysAlaSerLysLysLysArgSerSerAspLysLysLysSer 680
2295 TGTGGCGGTAGGAAGAGCAAGCAATCAAGAG--CGCTCGACAGAGAGAGTGC 2351
681 AsnLysHisValAspSerSerValProValPheAsnLeuGluAspIleGluGlyVal 700
2352 CAGAGCATGTGACAGTCTGTGCCAGTATTCACCTTGAAGATATAGAGGAGGAGTT 2411
701 GluGlyAlaGlyPheAspAspGluLysSerValLeuMetSerGlnMetSerLeuGluLys 720
2412 GAAGCGCTGGATTTCAGCAGCAGGAATCACTTCTATGTCTCAATGAGCCCTGGAGAAG 2471
721 ArgPheGlyGlnSerAlaAlaPheValAlaSerThrLeuMetGluTyrGlyGlyValPro 740
2472 AGATTTGGCCAGTCCGAGCGGTTTGTGCTCCACTCTGATGAGTATGTTGTTCTCT 2531
741 GlnSerSerThrProGluSerLeuLeuLysGluAlaIleHisValIleSerCysGlyTyr 760
2532 CACTCGCAACTCGAGTCTCTTCTGAAGAAGCTATCTATGTTATTAAGCTGTGGCTAT 2591
761 GluAspLysSerGluTyrGlyThrGluIleGlyTyrIleTyrGlySerValThrGluAsp 780
2592 GAGGACAAGACTGAATGGGAACCTGAGATCGGTGATCTACGGTCTGTGACAGAGAC 2651
781 IleLeuThrGlyPheLysMetHisAlaArgGlyTyrArgSerValTyrCysMetProLys 800
2652 ATTTCTACCGGATTCAGATGACCGCGAGGCTGGCGTGCATCTACTGCATGCCCAAG 2711
801 ArgProAlaPheLysGlySerAlaProIleAsnLeuSerAspArgLeuAsnGlnValLeu 820
2712 CGGCCAGCTTCAAGGGTCTGCCCCCATCAATCTTTTCGACCGCTCTGACACCATACCCG 2771
821 ArgTyrAlaLeuGlySerValGluIleLeuPheSerArgHisCysProLeuTyrTyrGly 840
2772 CGGTGGGCTCTGGGTCCGGAGATCCTCTTCAGCCGACCTGCCCTGTGTACGGC 2831
841 TyrGlyGlyArgLeuLysPheLeuGluArgPheAlaTyrIleAsnThrThrIleTyrPro 860
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861 LeuThrSerLeuProLeuValTyrCysIleLeuProAlaIleCysLeuLeuThrGly 880
2892 CTCACGTCCATCCGCTCTCTACTACTGATCTGCCGCACTCTGTCTGCTACCGGA 2951
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2952 AAGTTTCATATCCAGATCAGCACTTCGCGAGCATCTGTTTCATCTCCCTCTTCATC 3011
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921 TtpArgAsnGluGlnPheThrValIleGlyIleSerAlaHisLeuPheAlaValPhe 940

3072 TCGAGGAACGACGAGCTTCTGGGTGATCGGGGCATCTCCGGCACCTCTTCGCCGTGTC 3131
941 GlnGlyLeuLeuLysValLeuAlaGlyIleAspThrAsnPheThrValThrSerLysAla 960
3132 CAGGSCCTGCTCAAGAGTCTGCGCGCATCGACACCACTTCACCGTCACCTCCAGGCC 3191
961 AsnAspGluGluGlyAspPheAlaGluLeuTyrMetPheLysTyrThrThrLeuLeuIle 980
3192 TCGGACGAGGACGGGACTTCGCGAGCTGTACATGTTCAAGTGGACGACGCTCTCTGATC 3251
981 ProProThrThrIleLeuIleAsnMetValGlyValValAlaGlyThrSerTyrAla 1000
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3312 ATCAACGCGGATACCACTGTCGGGCGCTCTTCGCAAGCTCTTCTTCGCTCTCTGG 3371
1021 ValIleValHisLeuTyrProPheLeuLysGlyLeuMetGlyArgGlnAsnArgThrPro 1040
3372 GTATCTGTCACCTGTACCCGTTCTCAAGGCGCTCATGGCAGGCAACCGCACCCCG 3431
1041 ThrIleValIleValTyrAlaValLeuAlaSerIlePheSerLeuLeuTyrValArg 1060
3432 ACCATCGTCGTCGTCTGGGCACTCTGTCGGGCTCCATCTTCTCTGCTGTGGGTTCG 3491
1061 ValAspProPheThrThrArgLeuAlaGlyProAsnIleGlnThrCysGlyIleAsnCys 1080
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RESULT 4

AAZ95627

ID AAZ95627 standard; DNA; 3746 BP.

XX AAZ95627

AC AAZ95627

XX AAZ95627

DT 03-JUL-2000 (first entry)

XX DNA encoding a maize cellulose synthase.

DE Maize; cellulose synthase; stalk quality; stand; silage; cellulose;

KW transgenic plant; plant breeding marker; ss.

KW Zea mays.

XX Key

XX Location/Qualifiers

XX 321..3449

XX /tag= a

XX /product= "cellulose synthase"

XX /transl_except= (pos: 1800..1802, aa: Xaa)

XX /note= "no termination codon given; Xaa is an unspecified

XX amino acid"

XX WO200009706-A2.

XX 24-FEB-2000.

XX 16-AUG-1999; 99WO-US018760.

XX 17-AUG-1998; 98US-0096822P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Dhugga KS, Helentjaris TG, Bowen BA, Wang X;

XX WP1; 2000-224343/19.

XX P-PSDE; AAY84119.

XX New genes which encode maize cellulose synthase polypeptides in plants

XX useful for modulating the expression of cellulose synthase in plants and

XX to produce transgenic plants expressing the novel protein.

XX Claim 1; Page 176-181; 119pp; English.

XX PS